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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues

562222

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su Minimum DB seq length: 0 Maximum DB seq length: 2000000000

sp_archea:*
sp_bacteria:* sp_organelle:* sp_mhc:* sp_mammal:* sp_invertebrate:* sp_human:* sp_fungi:*

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summaries

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SUMMARIES

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SEQUENCE FROM N.A.

MEDILINE-97258620; PubMed=9104814;

MEDILINE-97258620; PubMed=9104814;

Lee S.Y., Choi Y.;

"TRAF-interacting protein (TRIP): a novel component of the tumor "TRAF-interacting protein (TRIP): and CD30-TRAF signaling complexes "necrosis factor receptor (INFR)- and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF kappaB activation.";

that inhibits TRAF2-1285(1997).

J. EX.P. Med. 185:1275-1285(1997).

J. EX.P. Med. 185:1275-1285(1997).

J. EX.P. Med. 185:2993.1;

-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

InterPro; IPR001841; Znf_ring.

Pfam; PF00097; zf-C3HC4; 1.

Pfam; PF00097; zf-C3HC4; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                    Zinc-finger.
SEQUENCE 469 AA; 53138 MW;
                                                                                                                                              SMART; SM00184; RING; 1.
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1 Similarity
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nilarity 96.1%;
Conservative
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pred. No. 1.2e-29;
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Q922M8;
Q922M8;
Q1-DEC-2001 (TrEMBLrel. 19, C
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Q1-DEC-2001 (TrEMBLrel. 19, L
TRAF-INTERACTING PROTEIN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Submitted (APR-2001)
EMBL; BC006929; AAH06
SEQUENCE 223 AA; 2
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ dat
-:- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; BC000310; AAH00310.1; -.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
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Mammalia; Eutheria;
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O1-JUN-2001 (TrEMBLrel. 17,

O1-DEC-2001 (TrEMBLrel. 19,
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Pred. No. 1.1e-28;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Jawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Nordone P., Ming B., Ringwald M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y.:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=EMBRYO
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"Functional annotation of a full-length mouse cDNA collection.";
"stuture 409:685-690(2001).
"I SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AK012948; BAB28567.1; -.
EMBL; AK012786; BAB28469.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Best Local
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                                                                                                                                                                       082372; PRELIMI
082372;
01-NOV-1998 (TrEMBL
01-NOV-1998 (TrEMBL
01-DEC-2001 (TrEMBL
ATZG29840 PROTEIN.
ATZG29840
SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embry,
Spermatophyta; Magnoliophyta; eddicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Three receptor genes for plasminogen related growth genome of the puffer fish Fugu rubripes.";
FEBS Lett. 443:370-374(1999).
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AJ010317; CAA09084.1; --
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-99148833; PubMed-10025966;
Cottage A.J., Clark M., Hawker K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.
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Zinc-finger.
470 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 AA;
                                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel.
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9 (TrEMBLrel. 10,
1 (TrEMBLrel. 19,
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76.08;
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                                                                                                                                                                                                              08,
19,
                                                                                 Brassicaceae;
                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 225; DB 13;
Pred. No. 8.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence up
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Pred. No. 1.4e-27;
o. wismatches 2;
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A8C31AAA4216E8C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                          core eudicots; Rosidae;
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RP SEQUENCE FROM N.A.

RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

RA Daganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.

RA Daganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.

RA Attix C., Andreise T., Trankheim M., Amico-Reiler G., Coefield J.,

RA Attix C., Andreise T., Trankheim M., Joon G., Kronmiller B.,

RA Attix C., Andreise T., Trankheim M., Jouan G., Kronmiller B.,

RA Attix C., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,

RA Attix C., Carrano A.V.;

RY Sequence analysis of a 2.5 Mb region in 19p13.3.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

2. InterPro. IPR000561; EGF-like.

2. InterPro. IPR000561; EGF-like.

2. InterPro. IPR0005137; PA.

2. InterPro. IPR0005137; PA.

3. Trankheim M., Skowronski E., Viswanathan V.,

RA Phan H., Viswanathan V., Skowronski E., Viswanathan V.,

RA Attix C., Andreise J., Andreise J., Carrano A.V.;

RA Attix C., Andreise T., Trankheim M., Andreise M., Store J., Andreise J., Carrano A.V.;

RA Attix C., Andreise T., Trankheim M., Andreise J., Ramire J., Andreise J.,
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01-NOV-1998
01-NOV-1998
             Zinc-finger
SEQUENCE
                                                  PROSITE; PS01186;
                                                                                       Pfam; PF00225; PA; 1.
Pfam; PF00097; zf-C3HC4; 1.
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                                                                                                                                   InterPro; IPR001841; Znf_ring
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
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-: SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
EMBL; AC005496; AAC35217.1; -.
HSSP; P28990; 1CHC.
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
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SEQUENCE 3
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les 19; Conserv
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                                                                            SM00184;
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8 (TrEMBLrel.
1 (TrEMBLrel.
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         ΑĄ,
                                RING; 1.
06; EGF_2; UNKNOWN_1.
         45880 MW;
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Pred. No. 1e-07;
1; Mismatches
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572731A8E8A97FCE CRC64;
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P STRAIN-BERKELEY;

XX MEDLINE-20196006; PubMed-10731132;

XX MEDLINE-20196006; PubMed-107, Ashburner M., Golle R.F.,

XX MEDLINE-20196006; PubMed-10731132;

XX MEDLINE-20196006; PubMed-10796006; PubMe
                                     RAA B B B RAA B 
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Best Local
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Q95SS5;
Q1-DEC-2001
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01-MAY-2000 (TrE
01-DEC-2001 (TrE
CG5140 PROTEIN.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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STRAIN-Y, CN BW SP;
STRAIN-Y, CN BW SP;
STRAIN-Y, CN BW SP;
Champe M., Brokstein P., Hong L., Agbayani A., Carlson J.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.
Schampe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg
Conzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY060610; AALJ28158.1;
SEQUENCE 435 AA; 48455 MW; OBFF0AC81DD9416E CRC64;
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01-DEC-2001
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Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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1 (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
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47
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9; Mismatches 21;
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Last sequence update)
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Pred. No. 1.5e-07;
6; Mismatches 15
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapheton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapheton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA Wang S.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.;
RT Telegence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
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Q9XZS4
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Query Match
Best Local S
Matches 21
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
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EMBL; AE003800; AAF57730.1;
   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Hongasha, Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Wartin J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M T Colling To The Training Market To Training Market
                                                                                                                                                                                                                                                                                                                                                                                                                                          EG:22E5.12 PROTEIN.
EG:22E5.12 OR CG4325.
EG:22E5.12 OR CG4325.
EUkaryota; melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-DEC-2001
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21; Conser
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Last sequence up
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Pred. No. 1.5e-07;
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                                                                                                         G.L.G.,
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D., Botchan

M.R.,

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RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.S., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McIntolv G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Ra Raizzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Raizzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Raizzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylore E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylore E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Yelson S.M., Woodseg T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang S.H., Zhong F.N., Zhong W., Zhou S., Zhao Q., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
RESULT
Q9M9UB
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Q9M9UB
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Q9M
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Q0M
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Matches 23
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Burtis K.C., Busam I
Cherry J.M., Cawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Murphy L., Harris D., Barrell B.;

"Sequencing the distal X chromosome of Drosophila melanogaster.";

submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9M9U8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00184; RING; 1. Zinc-finger.
                           Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicotyle eurosids II; Brassicales; Brassicaceae; NCBI_TaxID-3702;
                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                      F6A14.12 PROTEIN.
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23; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.5%;
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                                                                                                                                                                                                                                        15,
15,
                                                                  Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; Rosid Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB Pred. No. 7.2e 4; Mismatches
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Last sequence update)
Last annotation updat
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No. 7.
                                                                                                                                                                                                                                                                                                                                                    325
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.2e-08;
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Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                      Rosidae;
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RESULT 13
Q95RB5
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Q9N3D1
ID Q9
AC Q9
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DT 01
DT 01
DT 01
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GN Y1
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Best Local Similarity
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                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUROS S. Schwartz J. Shinn P. Toriumi M., Vysotskia Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (JAN-2000) to the EMBL/GenBank/DDJ databases.

-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AC011809; AAF27102.1; -
InterPro; IPR001664; IF.
InterPro; IPR001664; IF.
InterPro; IPR00184; Znf_ring.
Pfam; PF00097; zf-C3H04; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q95RB5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc-finger.
SEQUENCE 3
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                                                                                                                                                                                                                                                                               STRAIN=Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV061504; AAL29052.1;
                       Q9N3D1;
01-OCT-2000 (3
01-OCT-2000 (3
01-DEC-2001 (3
HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                       EMBL; AYO
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                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
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             Y54E10BR.3
                                                                                        Q9N3D1
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                                                                                                                                                                   3 LCTICSDFFDHSRDV--AAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                 14
                                                                                                                                                      18;
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                        0 (TrEMBLrel. 15, 0
0 (TrEMBLrel. 15, I
1 (TrEMBLrel. 19, I
NL 33.4 KDA PROTEIN
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                                                                                                                                                                                                                                                                        263 AA;
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                                                                                          PRELIMINARY;
                            KDA PROTEIN.
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                                                                                                                                                                                                                                                                          29515 MW;
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                                      Last sequence update)
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Pred. No. 2.1e-07;
                                                                  Created)
                                                                                                                                                                                                          Score 109.5; DB 5
Pred. No. 3.7e-07;
6; Mismatches 14
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Dunn P.,
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Caenorhabditis

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EMBL; AC024812; AAF59555.1; -
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3H64; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
Hypothetical protein; Zinc-finger.
Hypothetical protein; Zinc-finger.
SEQUENCE 304 AA; 33447 MW; 3E522361AAF54C44 CRC64;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tin-Wollam A., Becker M., Graves T.;
"The sequence of C. elegans cosmid Y54ElOBR.";
submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 39,6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston
                                                                                                                                                            STRAIN-NIPPONBARE;
de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
Nascimento L., Baker J., Vil M.D., Zutavern T., Santos L., Mille
Kuit K., Cunnius D.M., Rodriguez S., Balija V., Shah R., Bahret
Yang C., Bell M., Palmer L., O'Shaughessy A., Dedhia N.,
MCCombie W.R.;
"Genomic Sequence for Oryza sativa, Nipponbare strain, clone
"Genomic Sequence for Oryza sativa, Nipponbare strain, clone
"GSJNBA0067NO1, from chromosome 3, complete sequence.";
SJNBHO067NO1, to the EMBL/GenBank/DDBJ databases.
EMBL; AC090485; AAK98739.1; -.
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Oryza sativa (Rice).
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                                                                                                            Hypothetical protein SEQUENCE 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQCTTCFDTFKLDEDVGALDCNHIFHRPCIEPWLKT--KNSCPVCRQKV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAR-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.48;
                                                                                                                  39557 MW;
     37
     .1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107; DB 5;
Pred. No. 9.4e-07;
5; Mismatches 21;
     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                  ECF2CDC80C2E2DE1
     106; DB 10;
No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 304;
                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                    Miller B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      γ.
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RESULT Q9LT1L9 OC OC P P OC C P OC C P P OC C P P OC C P 
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065594
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
11-DEC-2001 (TrEMBLrel. 19, Last annotation update)
11- AUG-1998 (TrEMBLrel. 07, Created)
11- AUG-1998 (TrEMBLrel. 07, Last sequence update)
12- AUG-1998 (TrEMBLrel. 07, Last sequence update)
13- AUG-1998 (TrEMBLRel. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bevan M., Vandenbol M., Jallet C.,
Mewes H.W., Mayer K., Schueller C.,
Submitted (MAR-1998) to the EMBL/GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     065594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               065594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vandenbol M., Jallet C.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 65-344 FROM N.A.
ROSE M., Hempel S., Entian K.-D., Mewes H.W.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                            O9LT14 PRELIMINARY; PRT; 386 AA.

O9LT14:
01-OCT-2000 (TrEMBLrel 15, Created)
01-OCT-2000 (TrEMBLrel 15, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
GENOMIC DUA, CHROMOSOME 3, P1 CLONE: MPM9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta:
Spermatophyta; Magnoliophyta; eudicotyledons; core euerosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
         SEQUENCE FROM N.A
                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSICLDDFDKGSEAKEMPCKHKFHIRCIVPWLELHSS--CPVCRYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 38.1
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%;
38.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Portetelle D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 103; DB Pred. No. 3.8e 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mewes H.W., Lemcke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8e-06;
nes 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lemcke K., databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                           core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
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                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mayer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.F.X.;
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Best Local
                                                                                                                                                                       STRAIN-CV. COLUMBIA;
MEDLING-20083487; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Talion L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
                       -!- SIMILARITY: CONTAINS 1 RING-TYPE EMBL, AC005309; AACG3626.1; -. InterPro; IPR001841; Znf_ring. Pfam; PF00097; Zf-C3EC4; 1. SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotytaedons;
eurosids_II_Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                     STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                     AT2G47700 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 |
EMBL; AB025631; BAB01310.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=COLUMBIA;
MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-COLUMBIA;
Sato S., Nakamura Y., Kaneko T.,
                                                                                                                                                        Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      082239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1999)
                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 CAVCMDEFEDGSDVKQMPCKHVFHQDCLLPWLEL--HNSCPVCRFEL
             inc-finger
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                                                                                                                   COLUMBIA;
 324 AA;
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                                                                                                                               N.A.
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 35729 MW;
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Last annotation update)
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EMBL/GenBank/DDBJ databases
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 B3E836562546EA03 CRC64;
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                                                                            ZINC
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tches 21;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Havashitaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                             Matches
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Best Local
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Best Local
Q9LZ10
Q9LZ10;
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-!- SIMILARITY: CONTAINS
EMBL; AK005843; BAB24269
                                                                                                                                                                                                                                                                                           Pfam; PF00097; zf-C3HC4; SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                          HSSP; P28990; 1CHC
MGD; MGI:1341258;
                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                            PROSITE; PS01186; EGF_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                          InterPro; IPR000561; EGF-like InterPro; IPR001841; Znf_ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                               LCAICLDDYEEGERLKILPCAHAYHCRCIDPWFSRAAQRSCPLCKQSV
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l Similarity 41.3%;
19; Conservative
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001 (TrEMBLrel.
O SPECIFIC RING
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                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                            Ssrzfl
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Rodentia;
                                                                                                                                                                                                                                             35627 MW;
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17, 1
19, 1
ZINC
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                                                                                                                                                           Score 102; DB 11;
Pred. No. 4.9e-06;
9; Mismatches 23;
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Pred.
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                 PRT;
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No. 4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                            ZINC
                 274
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               ΑA
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                                                                                                                                                                                          Length 327;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 31.1 KDA PROTEIN.

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F9G14_60

Pred.

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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9M9U7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AL162973; CAB86029.1; -
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Terryn N., Ardiles W., Buysshaert C., Dassev
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den
Villaroel R., Gielen J., Van Montagu M., Bancroft I.,
Rudd S., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                HSSP; P28990, The state of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                  Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; ACOll809; AAF27103.1; -
                                                                                                                                                                                                                                                                        Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P. Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F6A14.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F6A14.13
     Zinc-finger.
SEQUENCE 2
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                                                                                                                                                   AC011809; AAI
P28990; 1CHC.
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O (TrEMBLrel.
1 (TrEMBLrel.
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274 AA; 31102 MW; 9A98B6C495A6F068
       224
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       Ą
                                                                                                   Znf_ring.
       26040
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15,
          MW.
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Last sequence update)
Last annotation update)
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Pred. No. 5.6e
6; Mismatches
          563926B745C61F8C
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No. 5
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          CRC64;
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Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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Den Daele H.,
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Query Match

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C TISSUE=GERMINATING PETUNIA POLLEN TREATED WITH KAEMPFER X MEDLINE=20317212; PubMed=10859200;

X MEDLINE=20317212; PubMed=10859200;

Y Govern V.N., Astwood J.D., Garner E.C., Dunker A.K., Tay, I solution and characterization of cDNAs expressed in tip of flavonol-induced pollen germination in petunia.";

Plant physiol. 123:699-710(2000).

REMBL, AF049930, AAD02556.1; -...

InterPro; IPR001841; Znf_ring.

SMARF; SM00184; RNG; 1.
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Matches 16; Conser
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Q9ZTM6;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2001
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Q9MAI1;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                              Kim C., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Lurz Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
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            -i- SIMILARITY: CONTAINS 1 RING
EMBL; AC008007; AAF69531.1; -.
INTEFPC; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                              Submitted (OCT-2000)
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Hansen N.F.,
                                                                                                                                                                                                                                                                                                     Davis R.W.,
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O1-MAY-1999 (TrEMBLrel. 10, Create of the control of the co
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SEQUENCE 5
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                                                                                                                                                                                                               Q9LTU8 PRELIMINARY; PRT; 325
Q9LTU8;
Q1-U8;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotate)
GB|AAF27103.1.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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Nature 400:532-538(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
SEQUENCE FROM N.A
                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001841; Znf_ring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCRIQV 50
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16; Conser
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Pred. No. 4.7e-05
2; Mismatches 1
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Pred. No. 2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsnith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
Q9LMT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, AT1G17970/F2H15_16.
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 7:131-135(2000).
-!- SIMILARITY: CONTAINS 1 |
EMBL; AB024034; BAB02789.1;
HSSP; P28990; 1CHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=COLUMBIA;
MEDLINE=20277480;
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Submitted (FEB-1999) t
                                                                                                                                                                                                                                                                                                                                                                   "Arabidopsis cDNA clones.";
Submitted (OCT-2001) to the
EMBL; AF428290; AAL16122.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta;
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                                                                                                        320 CSICQDEYEREDEVGELNCGHSFHVHCVKQWL--SRKNACPVCK
                                                                                                                                                                                                                                                       Local
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18; Conser
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15; Conserv
                                                                                                                                                                                                                                                                                                                                                  368 AA;
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                                                                                                                                                                                                                                                                                                                                                16122.1; -.
41618 MW;
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Pred. No. 1.7e
10; Mismatches
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EMBL/GenBank/DDBJ
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Pred. No.
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1.7e-05;
                                                                                                                                                                                                                                                       2e-05;
                                                                                                                                                                                                                                                                            DB 10;
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"The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-- SINILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AC034106; AAF97276.1;
InterPro; IPR0018A1 ***
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, P1 CLONE:MCD7.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Zince 383 AA;
                                                                                                     SEQUENCE
                                                                                                                          SMART; SM00184; RING;
Zinc-finger.
                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5 Sequence features of the regions of 1,456,315 bp covered physically assigned Pl and TAC clones."; DNA Res. 5:41-54(1998).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=COLUMBIA;
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RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Sutton G.G., Wortman J.R., Yandell M.D., Pfeiffer B.D.,
RA Barlow R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlow R.M., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrill J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davles P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.D., Mcherson D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.D., Mcherson D.,
RA Mount S.M., Mutphy B., Murphy L.M., Mcherson D.,
RA Nelson D.R., Pacleb J.M.,
RA Nelson D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rahen R., Ra Rahen R., Barkin R.,
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Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                         Q9FFB6;
Q9FFB6;
Q1-MAR-2001 (TrEMBLrel. 16, Careated)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PGPD14 PROTEIN (AT5G22920/MRN17_15).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantee; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
                                                                                                                                                                                                                                MEDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y.,
Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

SMBL; AYG60677; AAL28225.1; -.

SEQUENCE 626 AA; 69272 MW; F881B88D51D724EC CRC64;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                            "Structural analysis
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FFB6
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Q95SP2;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG1937
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                                                                                                                                                                Lones
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19; Conserv
                                                                                                                                                                     ral analysis of Arabidopsis thaliana chromosome of the 1.6 Mb regions covered by twenty physica s.".
                                                                                                                                 4:215-230(1997).
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1 (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Pred. No. 3.4e
8; Mismatches
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Last sequence update)
Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                             Kaneko T., Asamizu E.,
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. 3.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 626;
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                                                                                                                                                                               Query Match
Best Local
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Best Local S
Matches 17
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A Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
A Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
A Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Theologis cDNA clones.";
C "Arabidopsis cDNA clones.";
A L Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARTY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AB005243; BAB10613.1;
R EMBL; AB005243; BAB10613.1;
R EMBL; AV552362; AAK96553.1;
R InterPro; IPR001841; Znf.ring.
DR InterPro; IPR001841; Znf.ring.
DR Ffam; PP00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P15919; IRMD.

MGD; MGI:2137353; Trim7.

InterPro; IPR000315; Znf_bbox.

InterPro; IPR001841; Znf_ring.

Pfam; PF00643; Zf-B_box; 1.

Pfam; PF00097; Zf-G3HC4; 1.

PRINTS; PR01406; BBOXZNEINGER.

SMART; SM00336; BBOX; 1.

SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRIM7.

TRIM7.

Mus musculus (Mouse).

Mus musculus (Mouse).

Trim7.

Mus musculus (Mouse).

Musculus (Mouse).

Trim7.

Trim7.
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Q99PQ5,
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence up
O1-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=21231161; PubMed=11331580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger.
291 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karlin-Neumann G., Kawai J., Lam B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CTICSDF-FDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQC
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2
ATCSICLEFF---REPVSVECGHSFCRACIMRCWERPGAGTGTATRTLPCPLPCPQCR
                                                                   ALCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRT---
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                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                              243
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                    27256 MW;
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                                                                                                                                             12;
                                                                                                                                   Score 96.5; I
Pred. No. 2.16
l2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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Pred. No. 2.1e-05;
B; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                 284F3D48E8EEC781 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merla G., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Lee J.M.,
Onodera C.S
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nes 12;
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on update)
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Palm C.J.,
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RESULT
Q94GW2
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Q9M4C5
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Best Local S
Matches 18
                                                                                                Query Match
Best Local S
Matches 18
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE VIP2 PROTEIN.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-20208057; PubMed-10743654;

MEDLINE-20208057; PubMed-10743654;

Jones H.D., Kurup S., Peters N.C.B., Holdsworth M.J.;

Jones H.D., Kurup S., Peters N.C.B., Holdsworth M.J.;

Jones H.D., Kurup S., Peters N.C.B., Holdsworth M.J.;

Jentification and analysis of proteins that interact with the Avena fatua homologue of the maize transcription factor VIVIPAROUS 1.";

Plant J. 21:133-142(2000).

-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

EMBL; AJZ51051; CAB75506.1; -.

TRANSFAC; T04621; -.

InterPro; IPR001841; Znf_ring.

Pfam; PF00097; zf-C3HC4; 1.

SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S. Su C.-L., Chen C.-S., Shaw J.-F.;
"Oryza sativa PAC P0431G05 genomics sequence.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; ACO87551; AAK70903.1;
SEQUENCE 439 AA; 47922 MW; A8707375E3260893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q94GW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poeae; Avena.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIP2 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avena fatua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4499;
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                Zinc-finger
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                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSICLDAVVAAGGERSTARLQCGHEFHLDCIGSAFNAKGVMQCPNCR
CSICLDAVVAAAGGDRSTARLQCGHEFHLDCIGSAFNAKGVMQCPNCR
                                              CTICSDFF----DHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                      18;
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18; Conservative
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0 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                          442 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                          48184 MW;
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                                                                                                                                 33.6%;
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Last annotation update)
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Pred.
                                                                                                        Score 96; DB 10;
Pred. No. 4.4e-05;
; Mismatches 22;
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                                                                                                                                                                                                                                          441785914547281B CRC64;
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No. 3.
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                                                                                                                                                               Length 442;
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Best Local Similarity
Matches 18; Conserv
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Pfam; PF00643; zf-B_box; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIV "Prediction of the coding sequences of unidentified human genes. XIV "The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 6:197-205(1999).

DNA Res. 6:197-205(1999).

ENBL; ABD23021; BAAB3050.1; ".
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01-DEC-2001 (TrEMBLrel.
KIAA1098 PROTEIN (FRAGME
                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE RING ZINC FINGER PROTEIN.
AT4001270.
                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
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Mammalia; Eutheria;
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                                                            Lamar B.,
Mayer K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001870; Gamma_carbxylse
Interpro; IPR003877; SPRY.
Interpro; IPR003815; Znf_bbox.
Interpro; IPR001841; Znf_ring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EU Arabidopsis sequencing Submitted (MAR-2000) to the
                                                  Submitted
                                                                                       SEQUENCE FROM N.A.
                                                                                                              NCBI_TaxID=3702;
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     31
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                                                                                                                                                                                                                                                                                                                   LCAVCYDPF - - - RDAVTLRCGHNFCRGCVSRCWEVQVSPTCPVCK 72
                                                                                                                                                                                                                                                                                                                                        LCTICSDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTCPQCR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00518;
                                                               , Stoneking
F.X.;
                                                   (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AA;
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                         PRELIMINARY;
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EMBLrel. 13,
EMBLrel. 19,
4 (FRAGMENT).
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Primates;
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   ng project;
the EMBL/GenBank/DDBJ databases
                                                                             Stumpf J.,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                     Score 95.5; DB Pred. No. 6e-05; Mismatches
                                                    EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                           PRT;
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                                                                               Mewes
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                                                                               H.W.,
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RESULT
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AC OPEVID
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Silnn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA
Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
RA
Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA
Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA
Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA
Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA
Davis R.W., Theologis A., Ecker J.R.,
"Arabidopsis CDNA Clones.";
RI
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC
C1-: SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR
EMBL; AC005223; AAD10644.1; ...
DR
EMBL; AC039608; AAK62663.1; ...
DR
EMBL; AC039608; AAK62663.1; ...
DR
EMBL; AC09573; AAL1572.4; 1.
DR
EMBL; AC09097; Zf-C3HC4; 1.
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Best Local 9
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Q9ZVU8;
01-MAY-1999 (TIEMBLICAL 1
01-MAY-1999 (TIEMBLICAL 1
01-DEC-2001 (TIEMBLICAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lieuk K., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G.,

Rawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka

Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F. Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S. Lenz S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S. Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T5A14.7 PROTEIN (AT1G55530/T5A14_7).
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
Zinc-finger.
SEQUENCE 506 AA; 56518 MW; 1B06751A4E299FE8 C
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                   351 AA;
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10,
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Last
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Pred. No. 6e-05;
9; Mismatches 1
DE5ABB4D72CF7075 CRC64;
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Dunn P.,
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RESULT
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L Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
C -!- SIMIIARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
R EMBL; AL157474; CAB75669.1; -.
R EMBL; BC010369; AAH10369.1; -.
R Interpro; IPR001841; Znf_ring.
)R Pfam; PF00097; zf-C3H64; 1.
R SMART; SM00184; RING; 1.
KW HYPOTHETICAL PROTEIN; Zinc-finger.
SQ SEQUENCE 137 AA; 15739 MW; 6AA62DC6CEE8C114 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:P0480COl.";
                                                                                                            Spermatophyta; Magnoliophyta; Er
Ehrhartoideae; Oryzeae; Oryza, Liliopsida;
NCBI_TaxID-4530;
                                                                             SEQUENCE FROM
                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
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Q9NSR1;
Q1-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=AMYGDALA;
Ottenwaelder B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2000)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 15.7 KDA PROTEIN (LIKELY ORTHOLOG OF
DECEPT61D081.
                                                                                                                                                                                                                                                                                                                                                                                                                         85 CTICLSILEEGEDVRRLPCMHLFHQVCVDQWLIT---NKKCPICRVDI 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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17; Conser
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                            NIPPONBARE;
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36.2%;
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Primates;
                                                                                                                                                                                                                        19, Created)
19, Last sequence update)
19, Last annotation updat
(POLLEN GERMINATION RELAT
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                                Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 94; DB and Pred. No. 2.5e.
7; Mismatches
      genomic DNA,
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Pred. No. 4.8e
6; Mismatches
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Catarrhini; Hominidae;
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2.5e-05;
2.2;
                                                                                                                                                       Embryophyta; Tracheophyta;
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ches 21;
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                                                                                                                                          Poales;
    chromosome
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                                                                                                                                            Poaceae;
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                                                                                                                                                                                                                    PROTEIN).
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  PAC
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RESULT 40
Q90ZT8
ID Q90ZT8
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DE RING F
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Best Local Similarity 38.6%;
Matches 17; Conservative
Search completed: September Job time: 1492 sec
                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                          Query Match 32.9%;
Best Local Similarity 36.2%;
Matches 17; Conservative
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Q90ZT8;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RING FINGER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Induction of the mammalian node requires Arkadia function in the extraembryonic lineages.";
Nature 410:825-830(2001).
EMBL; AF329846; AAK38636.1; -.
NON_TER 1 1
NON_TER 1 1
SEQUENCE 879 AA; 95701 MW; EC8564B2280E3264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-21195971; PubMed-11298452;
Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARKADIA.
                                                                                                                                                                  PRELIMINARY;
                                                   4, 2002, 16:16:08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94; DB 10; Length 299;
pred. No. 5.6e-05;
9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                     Score 94; DB 13; Length 879; pred. No. 0.00017; pred. No. 0.10017; ndels
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